

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Griffith, Irwin J.
Pollock, Joanne

(ii) TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
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(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hohenschutz, Liza D.
(B) REGISTRATION NUMBER: 33,712
(C) REFERENCE/DOCKET NUMBER: IMPH-0001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215) 568-3100
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

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54 (A) ORGANISM: *Cryptomeria japonica*
55
56 (ix) FEATURE:
57 (A) NAME/KEY: CDS
58 (B) LOCATION: 66..1187
59
60 (ix) FEATURE:
61 (A) NAME/KEY: mat_peptide
62 (B) LOCATION: 129..1187
63
64
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67 AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACC 60
68
69 AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT 107
70 Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe
71 -21 -20 -15 -10
72
73 GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA 155
74 Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg
75 -5 1 5
76
77 GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA 203
78 Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala
79 10 15 20 25
80
81 GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GGA GAT CTT TAT 251
82 Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr
83 30 35 40
84
85 ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT 299
86 Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr
87 45 50 55
88
89 CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT 347
90 Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser
91 60 65 70
92
93 GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGG TAT 395
94 Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr
95 75 80 85
96
97 AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT 443
98 Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly
99 90 95 100 105
100
101 CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG 491
102 Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu
103 110 115 120
104
105 TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC 539
106 Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn

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107		125		130		135	
108							
109	GAG AGT TTT GGG GTG GAG CCT GTT CAT CCT CAG GAT GGC GAT GCT CTT						587
110	Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu						
111	140		145		150		
112							
113	ACT CTG CGC ACT GCT ACA AAT ATT TGG ATT GAT CAT AAT TCT TTC TCC						635
114	Thr Leu Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser						
115	155		160		165		
116							
117	AAT TCT TCT GAT GGT CTG GTC GAT GTC ACT CTT ACT TCG ACT GGA GTT						683
118	Asn Ser Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val						
119	170		175		180		185
120							
121	ACT ATT TCA AAC AAT CTT TTT TTC AAC CAT CAT AAA GTG ATG TTG TTA						731
122	Thr Ile Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu						
123		190		195		200	
124							
125	GGG CAT GAT GAT GCA TAT AGT GAT GAC AAA TCC ATG AAG GTG ACA GTG						779
126	Gly His Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val						
127		205		210		215	
128							
129	GCG TTC AAT CAA TTT GGA CCT AAC TGT GGA CAA AGA ATG CCC AGG GCA						827
130	Ala Phe Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala						
131		220		225		230	
132							
133	CGA TAT GGA CTT GTA CAT GTT GCA AAC AAT AAT TAT GAC CCA TGG ACT						875
134	Arg Tyr Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr						
135		235		240		245	
136							
137	ATA TAT GCA ATT GGT GGG AGT TCA AAT CCA ACC ATT CTA AGT GAA GGG						923
138	Ile Tyr Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly						
139		250		255		260	265
140							
141	AAT AGT TTC ACT GCA CCA AAT GAG AGC TAC AAG AAG CAA GTA ACC ATA						971
142	Asn Ser Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile						
143		270		275		280	
144							
145	CGT ATT GGA TGC AAA ACA TCA TCA TCT TGT TCA AAT TGG GTG TGG CAA						1019
146	Arg Ile Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln						
147		285		290		295	
148							
149	TCT ACA CAA GAT GTT TTT TAT AAT GGA GCT TAT TTT GTA TCA TCA GGG						1067
150	Ser Thr Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly						
151		300		305		310	
152							
153	AAA TAT GAA GGG GGT AAT ATA TAC ACA AAG AAA GAA GCT TTC AAT GTT						1115
154	Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val						
155		315		320		325	
156							
157	GAG AAT GGG AAT GCA ACT CCT CAA TTG ACA AAA AAT GCT GGG GTT TTA						1163
158	Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu						
159	330		335		340		345

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160
161 ACA TGC TCT CTC TCT AAA CGT TGT TGATGATGCA TATATTCTAG CATGTTGTAC 1217
162 Thr Cys Ser Leu Ser Lys Arg Cys
163 350
164
165 TATCTAAATT AACATCAACA AGAAAATATA TCATGATGTA TATTGTTGTA TTGATGTCAA 1277
166
167 AATAAAAATG TATCTTTTAC TATTAAAAAA AAAAATGATC GATCGGACGG TACCTCTAGA 1337
168
169
170
171 (2) INFORMATION FOR SEQ ID NO:2:
172
173 (i) SEQUENCE CHARACTERISTICS:
174 (A) LENGTH: 374 amino acids
175 (B) TYPE: amino acid
176 (D) TOPOLOGY: linear
177
178 (ii) MOLECULE TYPE: protein
179
180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
181
182 Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe Val Ile
183 -21 -20 -15 -10
184
185 Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp
186 -5 1 5 10
187
188 Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val Gly
189 15 20 25
190
191 Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr Thr Val
192 30 35 40
193
194 Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr Leu Arg
195 45 50 55
196
197 Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser Gly Asn
198 60 65 70 75
199
200 Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr
201 80 85 90
202
203 Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro Cys
204 95 100 105
205
206 Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu Tyr Leu
207 110 115 120
208
209 Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn Glu Ser
210 125 130 135
211
212 Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu Thr Leu

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213 140 145 150 155
214
215 Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser Asn Ser
216 160 165 170
217
218 Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val Thr Ile
219 175 180 185
220
221 Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His
222 190 195 200
223
224 Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe
225 205 210 215
226
227 Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr
228 220 225 230 235
229
230 Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr Ile Tyr
231 240 245 250
232
233 Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn Ser
234 255 260 265
235
236 Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile Arg Ile
237 270 275 280
238
239 Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln Ser Thr
240 285 290 295
241
242 Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr
243 300 305 310 315
244
245 Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu Asn
246 320 325 330
247
248 Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu Thr Cys
249 335 340 345
250
251 Ser Leu Ser Lys Arg Cys
252 350
253

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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266 GAYAAAYCCNA THGAYWS 17
267
268 (2) INFORMATION FOR SEQ ID NO:4:
269
270 (i) SEQUENCE CHARACTERISTICS:
271 (A) LENGTH: 25 base pairs
272 (B) TYPE: nucleic acid
273 (C) STRANDEDNESS: single
274 (D) TOPOLOGY: linear
275
276
277
278 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
279
280 GGGGAATTCAA YTGGGCNCAR AAYSG 25
281
282 (2) INFORMATION FOR SEQ ID NO:5:
283
284 (i) SEQUENCE CHARACTERISTICS:
285 (A) LENGTH: 23 base pairs
286 (B) TYPE: nucleic acid
287 (C) STRANDEDNESS: single
288 (D) TOPOLOGY: linear
289
290
291 (ix) FEATURE:
292 (A) NAME/KEY: modified_base
293 (B) LOCATION: 15
294 (D) OTHER INFORMATION: /mod_base= i
295
296
297 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
298
299 CTGCAGCCRT TYTCNACRTT RAA 23
300
301 (2) INFORMATION FOR SEQ ID NO:6:
302
303 (i) SEQUENCE CHARACTERISTICS:
304 (A) LENGTH: 20 base pairs
305 (B) TYPE: nucleic acid
306 (C) STRANDEDNESS: single
307 (D) TOPOLOGY: linear
308
309
310 (ix) FEATURE:
311 (A) NAME/KEY: modified_base
312 (B) LOCATION: 6
313 (D) OTHER INFORMATION: /mod_base= i
314
315
316 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
317
318 TTCATNCKRT TYTGNGCCCA 20

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319
320 (2) INFORMATION FOR SEQ ID NO:7:
321
322 (i) SEQUENCE CHARACTERISTICS:
323 (A) LENGTH: 25 base pairs
324 (B) TYPE: nucleic acid
325 (C) STRANDEDNESS: single
326 (D) TOPOLOGY: linear
327
328
329
330 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
331
332 CCTGCAGCKR TTYTGNGCCC AARTT 25
333
334 (2) INFORMATION FOR SEQ ID NO:8:
335
336 (i) SEQUENCE CHARACTERISTICS:
337 (A) LENGTH: 18 base pairs
338 (B) TYPE: nucleic acid
339 (C) STRANDEDNESS: single
340 (D) TOPOLOGY: linear
341
342
343
344 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
345
346 ATGGATTCCC CTTGCTTA 18
347
348 (2) INFORMATION FOR SEQ ID NO:9:
349
350 (i) SEQUENCE CHARACTERISTICS:
351 (A) LENGTH: 26 base pairs
352 (B) TYPE: nucleic acid
353 (C) STRANDEDNESS: single
354 (D) TOPOLOGY: linear
355
356
357
358 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
359
360 GGGAATTCGA TAATCCCATTA GACAGC 26
361
362 (2) INFORMATION FOR SEQ ID NO:10:
363
364 (i) SEQUENCE CHARACTERISTICS:
365 (A) LENGTH: 17 base pairs
366 (B) TYPE: nucleic acid
367 (C) STRANDEDNESS: single
368 (D) TOPOLOGY: linear
369
370
371

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372 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

373

374 ATGCCTATGT ACATTGC

17

375

376 (2) INFORMATION FOR SEQ ID NO:11:

377

378 (i) SEQUENCE CHARACTERISTICS:

379 (A) LENGTH: 17 base pairs

380 (B) TYPE: nucleic acid

381 (C) STRANDEDNESS: single

382 (D) TOPOLOGY: linear

383

384

385

386 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

387

388 GCAATGTACA TAGGCAT

17

389

390 (2) INFORMATION FOR SEQ ID NO:12:

391

392 (i) SEQUENCE CHARACTERISTICS:

393 (A) LENGTH: 18 base pairs

394 (B) TYPE: nucleic acid

395 (C) STRANDEDNESS: single

396 (D) TOPOLOGY: linear

397

398

399

400 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

401

402 TCCAATTCTT CTGATGGT

18

403

404 (2) INFORMATION FOR SEQ ID NO:13:

405

406 (i) SEQUENCE CHARACTERISTICS:

407 (A) LENGTH: 18 base pairs

408 (B) TYPE: nucleic acid

409 (C) STRANDEDNESS: single

410 (D) TOPOLOGY: linear

411

412

413

414 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

415

416 TTTTGTCAAT TGAGGAGT

18

417

418 (2) INFORMATION FOR SEQ ID NO:14:

419

420 (i) SEQUENCE CHARACTERISTICS:

421 (A) LENGTH: 30 base pairs

422 (B) TYPE: nucleic acid

423 (C) STRANDEDNESS: single

424 (D) TOPOLOGY: linear

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425
426
427
428 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
429
430 CCTGCAGAAG CTTTCATCAAC AACGTTTAGA 30
431
432 (2) INFORMATION FOR SEQ ID NO:15:
433
434 (i) SEQUENCE CHARACTERISTICS:
435 (A) LENGTH: 18 base pairs
436 (B) TYPE: nucleic acid
437 (C) STRANDEDNESS: single
438 (D) TOPOLOGY: linear
439
440
441
442 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
443
444 TAGAACTCCA GTCGAAGT 18
445
446 (2) INFORMATION FOR SEQ ID NO:16:
447
448 (i) SEQUENCE CHARACTERISTICS:
449 (A) LENGTH: 17 base pairs
450 (B) TYPE: nucleic acid
451 (C) STRANDEDNESS: single
452 (D) TOPOLOGY: linear
453
454
455
456 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
457
458 TAGCTCTCAT TTGGTGC 17
459
460 (2) INFORMATION FOR SEQ ID NO:17:
461
462 (i) SEQUENCE CHARACTERISTICS:
463 (A) LENGTH: 18 base pairs
464 (B) TYPE: nucleic acid
465 (C) STRANDEDNESS: single
466 (D) TOPOLOGY: linear
467
468
469
470 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
471
472 TATGCAATTG GTGGGAGT 18
473
474 (2) INFORMATION FOR SEQ ID NO:18:
475
476 (i) SEQUENCE CHARACTERISTICS:
477 (A) LENGTH: 20 amino acids

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478 (B) TYPE: amino acid
479 (D) TOPOLOGY: linear
480
481 (ii) MOLECULE TYPE: peptide
482
483 (v) FRAGMENT TYPE: N-terminal
484
485 (vi) ORIGINAL SOURCE:
486 (A) ORGANISM: *Cryptomeria japonica*
487
488 (ix) FEATURE:
489 (A) NAME/KEY: Modified-site
490 (B) LOCATION: 7
491 (D) OTHER INFORMATION: /note= "the amino acid at position
492 7 is Ser, Cys, Thr, or His"
493
494
495 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
496
497 Asp Asn Pro Ile Asp Ser Xaa Trp Arg Gly Asp Ser Asn Trp Ala Gln
498 1 5 10 15
499
500 Asn Arg Met Lys
501 20
502
503 (2) INFORMATION FOR SEQ ID NO:19:
504
505 (i) SEQUENCE CHARACTERISTICS:
506 (A) LENGTH: 16 amino acids
507 (B) TYPE: amino acid
508 (D) TOPOLOGY: linear
509
510 (ii) MOLECULE TYPE: peptide
511
512 (v) FRAGMENT TYPE: internal
513
514 (vi) ORIGINAL SOURCE:
515 (A) ORGANISM: *Cryptomeria japonica*
516
517
518 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
519
520 Glu Ala Phe Asn Val Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys
521 1 5 10 15
522
523
524 (2) INFORMATION FOR SEQ ID NO:20:
525
526 (i) SEQUENCE CHARACTERISTICS:
527 (A) LENGTH: 30 base pairs
528 (B) TYPE: nucleic acid
529 (C) STRANDEDNESS: single
530 (D) TOPOLOGY: linear

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531
532
533
534 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
535
536 GGGTCTAGAG GTACCGTCCG ATCGATCATT 30
537
538 (2) INFORMATION FOR SEQ ID NO:21:
539
540 (i) SEQUENCE CHARACTERISTICS:
541 (A) LENGTH: 20 base pairs
542 (B) TYPE: nucleic acid
543 (C) STRANDEDNESS: single
544 (D) TOPOLOGY: linear
545
546
547
548 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
549
550 GGGTCTAGAG GTACCGTCCG 20
551
552 (2) INFORMATION FOR SEQ ID NO:22:
553
554 (i) SEQUENCE CHARACTERISTICS:
555 (A) LENGTH: 13 base pairs
556 (B) TYPE: nucleic acid
557 (C) STRANDEDNESS: single
558 (D) TOPOLOGY: linear
559
560
561
562 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
563
564 AATGATCGAT GCT 13
565
566 (2) INFORMATION FOR SEQ ID NO:23:
567
568 (i) SEQUENCE CHARACTERISTICS:
569 (A) LENGTH: 21 base pairs
570 (B) TYPE: nucleic acid
571 (C) STRANDEDNESS: single
572 (D) TOPOLOGY: linear
573
574
575
576 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
577
578 GGAATTCTCT AGACTGCAGG T 21
579
580 (2) INFORMATION FOR SEQ ID NO:24:
581
582 (i) SEQUENCE CHARACTERISTICS:
583 (A) LENGTH: 35 base pairs

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584 (B) TYPE: nucleic acid
585 (C) STRANDEDNESS: single
586 (D) TOPOLOGY: linear
587
588
589

590 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

591
592 GGAATTCTCT AGACTGCAGG TTTTTTTTTT TTTT
593

35

594 (2) INFORMATION FOR SEQ ID NO:25:

595
596 (i) SEQUENCE CHARACTERISTICS:
597 (A) LENGTH: 5 amino acids
598 (B) TYPE: amino acid
599 (D) TOPOLOGY: linear
600

601 (ii) MOLECULE TYPE: peptide
602

603 (v) FRAGMENT TYPE: N-terminal
604

605 (vi) ORIGINAL SOURCE:

606 (A) ORGANISM: Juniperus sabinoides
607
608

609 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

610
611 Asp Asn Pro Ile Asp
612 1 5

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/730,452

DATE: 07/22/91
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ORIGINAL TEXT

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/730,452

DATE: 07/22/91
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MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/730,452

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CORRECTED TEXT